AMENDMENTS TO THE SPECIFICATION:

Please replace the paragraph at page 6 lines 11 to page 7 line 3 of the substitute specification submitted on February 24, 2003 with the following:

- International Application WO 95/31557 which describes a transfection vector comprising a synthetic peptide and the nucleic acid to be transfected. The synthetic peptide comprises a polymeric chain of basic amino acids, preferably at the C-terminal position (10-50 amino acids, such as lysine, arginine and ornithine), an NLS peptide (6-15 amino acids, such as the NLS sequence of the SV40 T antigen, the NLS sequence of the polyoma T antigen, the NLS sequence of adenovirus E1a or the NLS sequence of adenovirus E1b, preferably at the N-terminal position and a hinge region of neutral amino acids (6-50 amino acids selected from glycine, alanine, leucine and isoleucine), between the polymeric chain and the NLS peptide. The preferred NLS sequence is the sequence of the SV40 virus T antigen (small sequence of basic amino acids: PKKKRKV SEQ ID NO: 25), which is efficient in mammalian cells or a short hydrophobic sequence which contains one or more basic amino acids (KIPIK SEQ ID NO:43). The hinge sequence comprises 6-26 neutral amino acids selected solely from Gly (G), Ala (A), Leu (L) and Ile (I). The peptide:DNA ratio (by weight) is between 1:1 and 1:10. The peptide described in this document passes across the cell membrane with difficulty and that is the reason why it is recommended, in this International Application, to treat the cells before the transfection: the cells are treated with a hypertonic solution, and then with a hypotonic solution in the presence of the nucleic acid-peptide complex. The hypertonic solution may contain PEG (0.3 M-0.6 M) and sucrose (10-25%).

Please replace TABLE 1 at page 20 of the substitute specification with the following:

TABLE I

Peptide	Sequences[*]
I	A K R A R L S T S F N P V Y P Y E D E S - K_{20} = SEQ ID NO:2 + SEQ ID NO:10 + SEQ ID NO:7 + SEQ ID NO:16-K_{20} (SEQ ID NO:44)
IC	A K R A R L S T S F N P V Y P Y E D E S - K_{10} = SEQ ID NO:2 + SEQ ID NO:10 + SEQ ID NO:7 + SEQ ID NO:16-K_{10} (SEQ ID NO:45)
IE	A K R A R L S T S E D E S-K_{10} = SEQ ID NO:2 + SEQ ID NO:10 + SEQ ID NO:16-K_{10} (SEQ ID NO:46)
ID	L S T S F N P V Y P Y E D E S-K_{20} = SEQ ID NO:10 + SEQ ID NO:7 + SEQ ID NO:16-K_{20} (SEQ ID NO:47)
IA	A K R A R L S T S F N P V Y P Y E D E S = SEQ ID NO:2 + SEQ ID NO:10 + SEQ ID NO:7 + SEQ ID NO:16 (SEQ ID NO:48)
LII	A K R A R L S T S F N P V Y P Y E D E S $\backslash$ K_{19} / A K R A R L S T S F N P V Y P Y E D E S (SEQ ID NO:49) (for each branch: SEQ ID NO:2 + SEQ ID NO:10 + SEQ ID NO:7 + SEQ ID NO:16)

* in which X_0 = A.